



SEQUENCE LISTING

RECEIVED
MAR 01 2001
TECH CENTER 1690/230

<110> Robison, Keith E.
Kapeller-Libermann, Rosana
White, David

<120> 22025, A Novel Human Cyclic Nucleotide
Phosphodiesterase

<130> 35800/204489

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<141> 2000-09-22

<150> 09/330,970
<151> 1999-06-11

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<212> PRT
<213> Homo sapiens

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35 40 45
Met Val Lys Leu Val Trp Lys Ser Lys Ser Glu Leu Gln Ala Thr Lys
50 55 60
Gln Arg Gly Ile Leu Asp Asn Glu Asp Ala Leu Arg Ser Phe Pro Gly
65 70 75 80
Asp Ile Arg Leu Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly
85 90 95
Ser Tyr Pro Phe Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser
100 105 110
Gly Glu Ile Gly Thr Lys Lys Val Lys Arg Leu Leu Ser Phe Gln
115 120 125
Arg Tyr Phe His Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala
130 135 140
Pro Leu His Leu Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met
145 150 155 160
Leu Ser Lys Val Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg
165 170 175
Leu Thr Asn Gly Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn
180 185 190
Thr His Gly Leu Ile His His Phe Lys Leu Asp Met Val Thr Leu His
195 200 205
Arg Phe Leu Val Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr
210 215 220
His Asn Ala Val His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr

225	230	235	240
Leu Lys Glu Pro Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met			
245	250	255	
Leu Gly Leu Leu Ala Ala Ala His Asp Val Asp His Pro Gly Val			
260	265	270	
Asn Gln Pro Phe Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr			
275	280	285	
Gln Asn Met Ser Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly			
290	295	300	
Met Leu Arg Glu Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr			
305	310	315	320
Gln Asp Ile Glu Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile			
325	330	335	
Asn Arg Gln Asn Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn			
340	345	350	
Lys Asp Leu Arg Leu Glu Asp Ala Gln Asp Arg His Phe Met Leu Gln			
355	360	365	
Ile Ala Leu Lys Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu			
370	375	380	
Met Ser Lys Gln Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln			
385	390	395	400
Gly Glu Leu Glu Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn			
405	410	415	
Gln Gln Lys Asp Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Ser Tyr			
420	425	430	
Ile Val Glu Pro Leu Phe Arg Glu Trp Ala His Phe Thr Gly Asn Ser			
435	440	445	
Thr Leu Ser Glu Asn Met Leu Gly His Leu Ala His Asn Lys Ala Gln			
450	455	460	
Trp Lys Ser Leu Leu Pro Arg Gln His Arg Ser Arg Gly Ser Ser Gly			
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Gln Glu Gly Asp Ser Pro			
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<213> Homo sapeins

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cacgcacgac agcagcagaa gcagaaaacag cagcagcagc aacagcagca gcagcagcag	180		
caccaccacc accactaccc cctcttctgg ggcacaagac aga atg cct gtg cta	235		
Met Pro Val Leu			
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gag cga tat ttc cac cca gca gag cta ggc agg agg tgg aca ggc cca	283		
Glu Arg Tyr Phe His Pro Ala Glu Leu Gly Arg Arg Trp Thr Gly Pro			
5	10	15	20

gaa ggt gtg ctg ccc tcc tcc ccg gga agc cg ²⁵ ggg tgc cag cag Glu Gly Val Leu Pro Ser Ser Pro Gly Ser Arg Pro Gly Cys Gln Gln 30 35	331
ggg ccg ctg ccc tgg gac ttg cca gag atg atc agg atg gta aag ctg Gly Pro Leu Pro Trp Asp Leu Pro Glu Met Ile Arg Met Val Lys Leu 40 45 50	379
gtt tgg aaa tcc aaa agt gag ctg cag gcg acc aaa cag aga ggc att Val Trp Lys Ser Lys Ser Glu Leu Gln Ala Thr Lys Gln Arg Gly Ile 55 60 65	427
ctg gac aat gaa gat gct ctc cgc agc ttt cca gga gat ata cga cta Leu Asp Asn Glu Asp Ala Leu Arg Ser Phe Pro Gly Asp Ile Arg Leu 70 75 80	475
agg ggt cag acg ggg gtt cgt gct gaa cgc cgt ggc tcc tac cca ttc Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly Ser Tyr Pro Phe 85 90 95 100	523
att gac ttc cgc cta ctt aac agt aca aca tac tca ggg gag att ggc Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser Gly Glu Ile Gly 105 110 115	571
acc aag aaa aag gtg aaa aga cta tta agc ttt caa aga tac ttc cat Thr Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His 120 125 130	619
gca tca agg ctg ctt cgt gga att ata cca caa gcc cct ctg cac ctg Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu 135 140 145	667
ctg gat gaa gac tac ctt gga caa gca agg cat atg ctc tcc aaa gtg Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val 150 155 160	715
gga atg tgg gat ttt gac att ttc ttg ttt gat cgc ttg aca aat gga Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly 165 170 175 180	763
aac agc ctg gta aca ctg ttg tgc cac ctc ttc aat acc cat gga ctc Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Thr His Gly Leu 185 190 195	811
att cac cat ttc aag tta gat atg gtg acc tta cac cga ttt tta gtc Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val 200 205 210	859
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cac gca gcc gac gtc acc cag gcc atg cac tgc tac ctg aaa gag cca His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro 230 235 240	955
aag ctt gcc agc ttc ctc acg cct ctg gac atc atg ctt gga ctg ctg	1003

Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu			
245	250	255	260
gct gca gca gca cac gat gtg gac cac cca ggg gtg aac cag cca ttt			1051
Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe			
265	270	275	
ttg ata aaa act aac cac cat ctt gca aac cta tat cag aat atg tct			1099
Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser			
280	285	290	
gtg ctg gag aat cat cac tgg cga tct aca att ggc atg ctt cga gaa			1147
Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu			
295	300	305	
tca agg ctt ctt gct cat ttg cca aag gaa atg aca cag gat att gaa			1195
Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu			
310	315	320	
cag cag ctg ggc tcc ttg atc ttg gca aca gac atc aac agg cag aat			1243
Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn			
325	330	335	340
gaa ttt ttg acc aga ttg aaa gct cac ctc cac aat aaa gac tta aga			1291
Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg			
345	350	355	
ctg gag gat gca cag gac agg cac ttt atg ctt cag atc gcc ttg aag			1339
Leu Glu Asp Ala Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys			
360	365	370	
tgt gct gac att tgc aat cct tgt aga atc tgg gag atg agc aag cag			1387
Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln			
375	380	385	
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Trp Ser Glu Arg Val Cys Glu Phe Tyr Arg Gln Gly Glu Leu Glu			
390	395	400	
cag aaa ttt gaa ctg gaa atc agt cct ctt tgt aat caa cag aaa gat			1483
Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp			
405	410	415	420
tcc atc cct agt ata caa att ggt ttc atg agc tac atc gtg gag ccg			1531
Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Ser Tyr Ile Val Glu Pro			
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ctc ttc cgg gaa tgg gcc cat ttc acg ggt aac agc acc ctg tcg gag			1579
Leu Phe Arg Glu Trp Ala His Phe Thr Gly Asn Ser Thr Leu Ser Glu			
440	445	450	
aac atg ctg ggc cac ctc gca cac aac aag gcc cag tgg aag agc ctg			1627
Asn Met Leu Gly His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu			
455	460	465	
ttg ccc agg cag cac aga agc agg ggc agc agt ggc agc ggg cct gac			1675
Leu Pro Arg Gln His Arg Ser Arg Gly Ser Ser Gly Ser Gly Pro Asp			

470

475

480

cac gac cac gca ggc caa ggg act gag agc gag gag cag gaa ggc gac 1723
 His Asp His Ala Gly Gln Gly Thr Glu Ser Glu Glu Gln Glu Gly Asp
 485 490 495 500

agc ccc tagggccgg cccaaacttag acgcggctct cctccggcag ggcccccaga 1779
 Ser Pro

ggcagaagg agcgtggagg ggcctcaccg cagcagccca gccacttct gagtgttgc 1839
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<213> Homo sapiens

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 Gly Cys Gln Gln Gly Pro Leu Pro Trp Asp Leu Pro Glu Met Ile Arg
 35 40 45
 Met Val Lys Leu Val Trp Lys Ser Lys Ser Glu Leu Gln Ala Thr Lys
 50 55 60
 Gln Arg Gly Ile Leu Asp Asn Glu Asp Ala Leu Arg Ser Phe Pro Gly
 65 70 75 80
 Asp Ile Arg Leu Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly
 85 90 95
 Ser Tyr Pro Phe Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser
 100 105 110
 Gly Glu Ile Gly Thr Lys Lys Val Lys Arg Leu Leu Ser Phe Gln
 115 120 125
 Arg Tyr Phe His Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala
 130 135 140
 Pro Leu His Leu Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met
 145 150 155 160
 Leu Ser Lys Val Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg
 165 170 175
 Leu Thr Asn Gly Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn
 180 185 190
 Thr His Gly Leu Ile His His Phe Lys Leu Asp Met Val Thr Leu His
 195 200 205
 Arg Phe Leu Val Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr
 210 215 220
 His Asn Ala Val His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr
 225 230 235 240
 Leu Lys Glu Pro Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met
 245 250 255

Leu Gly Leu Ala Ala Ala His Asp Val Asp His Pro Gly Val
 260 265 270
 Asn Gln Pro Phe Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr
 275 280 285
 Gln Asn Met Ser Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly
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 Met Leu Arg Glu Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr
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gccagcttcc	tcacgcctct	ggacatcatg	cttggactgc	tggctgcagc	agcacacgat	1020
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aaagagaaaa	ctgaaactgc	tagtaatcct	gccatccagg	tatagttcat	gttaacctgg	2820
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ataccactac	tgccttcat	ttggaattca	aatgtttcc	aatatccaa	actttgatac	3060
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aagtttcttg	tatattatcc	agttgttctt	ctaaaaggct	gtatctacct	gtattccaac	3180
tgtatggattt	taagaaaatg	taccaatgtt	ccatcaccaa	aattgagttt	atttttatct	3240
ttttaaaata	tttgcaaatt	tgacatatat	gtatgtat	acacaaatat	atatgtaaag	3300
tggttttcat	taaatttagta	tgcatcctt	acttac			3336

<210> 5

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence for 3'5'-Cyclic Nucleotide
Phosphodiesterase Family 7 from the Prosite
database

<400> 5

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															30
Leu	Ala	Leu	Val	Phe	Ala	Ala	Ala	Ile	His	Asp	Val	Asp	His	Arg	Gly
															45
Thr	Asn	Asn	Ser	Phe	Gln	Ile	Asn	Ser	Leu	Gln	Lys	Ser	Glu	Leu	Ala
															60
Leu	Leu	Tyr	Asn	Asp	Glu	Gly	Ser	Val	Leu	Glu	Asn	His	His	Leu	Ala
															80
Gln	Ala	Phe	Lys	Leu	Leu	Gln	Asp	Glu	Glu	Cys	Asn	Ile	Phe	Gln	Asn
															95
Leu	Ser	Lys	Lys	Asp	Phe	Arg	Thr	Leu	Arg	Asp	Leu	Val	Ile	Glu	Ala
															110
Ile	Leu	Ala	Thr	Asp	Met	Ser	Leu	His	Leu	Gln	Lys	Leu	Lys	Asp	Leu
															125
Lys	Thr	Met	Val	Glu	Gln	Lys	Lys	Val	Tyr	Glu	Thr	Gly	Val	Glu	Trp
															140
Thr	Gln	Tyr	Leu	Leu	Asp	Asn	Tyr	Thr	His	Lys	Ile	Leu	Leu	Ser	
															160
Leu	Leu	Met	Thr	Ala	Ala	Asp	Leu	Ser	Asn	Pro	Thr	Lys	Pro	Trp	Ser
															175
Leu	Ser	Lys	Arg	Trp	Ala	Glu	Leu	Ile	Met	Glu	Glu	Phe	Phe	Glu	Gln
															190
Gly	Asp	Leu	Glu	Arg	Glu	Leu	Gly	Leu	Asp	Arg	Pro	Ser	Pro	Met	Cys
															205

Asp Arg Thr Ser Ala Ala Tyr Val Pro Lys Ser Gln Val Gly Phe Ile
210 215 220
Asp Phe Ile Val Glu Pro Val Phe Lys Leu Leu Ala Asp Val Val Glu
225 230 235 240
Lys Gly Arg Thr Thr Ser Glu Ala Ile Asp Ala Asn His Leu Cys Trp
245 250 255
Val Ala Leu Asp Glu Glu Val Arg Asn Asp Asp Ile Ala Pro Leu Leu
260 265 270
Asp Arg Ile Glu Asp Asn Arg
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<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence for 3'5'-Cyclic Nucleotide
Phosphodiesterase Family 7 from the Prosite
database

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Leu Leu Leu Thr Leu Ala Leu Glu Arg Tyr Leu Thr Asp Leu Glu Val
20 25 30
Leu Ala Leu Val Phe Ala Ala Ala Ile His Asp Val Asp His Arg Gly
35 40 45
Thr Asn Asn Ser Phe Gln Ile Asn Ser Leu Gln Lys Ser Glu Leu Ala
50 55 60
Leu Leu Tyr Asn Asp Glu Gly Ser Val Leu Glu Asn His His Leu Ala
65 70 75 80
Gln Ala Phe Lys Leu Leu Gln Asp
85